

COPY OF PAPER
ORIGINALLY FILED



SEQUENCE LISTING

<110> Skeiky, Yasir
Guderian, Jeff
Corixa Corporation

<120> Methods of Using a Mycobacterium tuberculosis Coding Sequence to Facilitate Stable and High Yield Expression of Heterologous Proteins

<130> 014058-008010US

<140> US 09/684,215

<141> 2000-10-06

<150> US 60/158,585

<151> 1999-10-07

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 1872

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 32 KD serine protease MTB32A

<220>

<221> CDS

<222> (89)..(1156)

<223> MTB32A

<220>

<221> sig_peptide

<222> (89)..(184)

<223> N-terminal hydrophobic secretory signal sequence

<220>

<221> mat_peptide

<222> (185)..(1153)

<400> 1

gactacgttg gtgttagaaaa atcctgccgc ccggaccctt aaggctggga caatttctga 60

tagtacccca gacacaggag gttacggg atg agc aat tcg cgc cgc cgc tca 112
Met Ser Asn Ser Arg Arg Arg Ser
-30 -25

ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160
Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
-20 -15 -10

ctg gcc acg gcg ccg gcc cag gcg ccg ccg gcc ttg tcg cag gac 208
Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
-5 -1 1 5

RECEIVED

MAR 19 2002

TECH CENTER 1600/2900

cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc 256
 Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val
 10 15 20

 gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac 304
 Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr
 25 30 35 40

 aac aac gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt 352
 Asn Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly
 45 50 55

 gtc gtg ctg acc aac cac gtg atc gcg ggc gcc acc gac atc aat 400
 Val Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn
 60 65 70

 gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg 448
 Ala Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly
 75 80 85

 tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt 496
 Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly
 90 95 100

 ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc 544
 Gly Leu Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro
 105 110 115 120

 gtc gtc gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg 592
 Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala
 125 130 135

 gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat 640
 Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp
 140 145 150

 tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat 688
 Ser Leu Thr Gly Ala Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp
 155 160 165

 gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta 736
 Ala Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu
 170 175 180

 gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg 784
 Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu
 185 190 195 200

 tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg 832
 Ser Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 205 210 215

 atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc 880
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 220 225 230

 ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac 928
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 235 240 245

ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc	976		
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu			
250	255	260	
ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc	1024		
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile			
265	270	275	280
aac tcg gcc acc gcg atg gcg gac gct aac ggg cat cat ccc ggt	1072		
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly			
285	290	295	
gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca	1120		
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr			
300	305	310	
ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga ttgcgtcgcg	1156		
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala			
315	320		
gataccaccc gcccggccgc caattggatt ggccgcgcgtgattgccgcgtgagcccc	1226		
cgagttccgt ctcccgatcg cgtggcatcg tgaaagcaat gaacgaggca gaacacagcg	1286		
tgcagcaccc tcccgtcgag ggcagtcacg tcgaaggcggtgtggtcgag catccggatg	1346		
ccaaggactt cggcagcgcc gcccgcctgc ccggcgtatcc gacctggttt aagcacgccc	1406		
tcttctacga ggtgctggtc cggcggttct tcgacgcccag cgccggacgggt tccggcgtatc	1466		
tgcgtggact catcgatcgc ctgcactacc tgcagtggct tggcatcgac tgcacatctgg	1526		
tgcgcgcgtt ctacgactcg ccgctgcgcg acggcggtta cgacattcgc gacttctaca	1586		
aggtgtgccc cgaattcgcc accgtcgacg atttcgtcgccctggatcgac gccgctcacc	1646		
ggcggatcatc accgacactgg tgcacatcgac cacctggag tgcacccct	1706		
ggtttcagga gtcccgccgc gacccagacg gaccgtacgg tgactattac gtgtggagcg	1766		
acaccagcga gcgctacacc gacgccccga tcatcttcgt cgacacccgaa gagtcgaact	1826		
ggtcattcga tcctgtccgc cgacagttct actggcaccg attctt	1872		

<210> 2

<211> 355

<212> PRT

<213> Mycobacterium tuberculosis

<223> 32 KD serine protease MTB32A

<400> 2

Met Ser Asn Ser Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser			
1	5	10	15
Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala			
20	25	30	
Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu			
35	40	45	
Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val			
50	55	60	

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

<210> 3
 <211> 396
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ra12

<220>
 <221> CDS
 <222> (1)...(396)
 <223> Ra12

<400> 3
 acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag gga ttc 48
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15

gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg 96
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30

ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc	144
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly	
35 40	45
ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg	192
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val	
50 55	60
gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg	240
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val	
65 70	75 80
atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg	288
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala	
85 90	95
gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg	336
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp	
100 105	110
caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag	384
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu	
115 120	125
gga ccc ccc gcc	396
Gly Pro Pro Ala	
130	
<210> 4	
<211> 132	
<212> PRT	
<213> Mycobacterium tuberculosis	
<223> 14 KD C-terminal fragment of MTB32A Ra12	
<400> 4	
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gln Gly Phe	
1 5 10 15	
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser	
20 25 30	
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly	
35 40 45	
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val	
50 55 60	
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val	
65 70 75 80	
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala	
85 90 95	
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp	
100 105 110	
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu	
115 120 125	
(Gly Pro Pro Ala)	
130	
<210> 5	
<211> 702	
<212> DNA	
<213> Artificial Sequence	

ccc ctc ccc ggc ccg ccg cca ccg ggt ggt tgc ggt ggg gca att ccg 672
Pro Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro
210 215 220

tcc gag cag ccc aac gct ccc tga gaattc 702
Ser Glu Gln Pro Asn Ala Pro
225 230

<210> 6
<211> 230

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:Ra12-DPPD fusion polypeptide

<400> 6
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
35 40 45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp Asp
130 135 140
Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr
145 150 155 160
Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly
165 170 175
Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp
180 185 190
Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro
195 200 205
Leu Pro Gly Pro Pro Pro Gly Gly Cys Gly Ala Ile Pro Ser
210 215 220
Glu Gln Pro Asn Ala Pro
225 230

<210> 7
<211> 1746

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12-WT1 fusion

<220>
<221> CDS

<222> (4)..(1740)

<223> Ra12-WT1 fusion polypeptide

gca ttc acc gtt cac ttc tcc ggc cag ttc act ggc aca gcc gga gcc Ala Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala 240 245 250 255	768
tgt cgc tac ggg ccc ttc ggt cct cct ccg ccc agc cag ggc tca tcc Cys Arg Tyr Gly Pro Phe Gly Pro Pro Pro Ser Gln Ala Ser Ser 260 265 270	816
ggc cag gcc agg atg ttt cct aac gcg ccc tac ctg ccc agc tgc ctc Gly Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu 275 280 285	864
gag agc cag ccc gct att cgc aat cag ggt tac agc acg gtc acc ttc Glu Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe 290 295 300	912
gac ggg acg ccc agc tac ggt cac acg ccc tcg cac cat gcg gcg cag Asp Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln 305 310 315	960
ttc ccc aac cac tca ttc aag cat gag gat ccc atg ggc cag cag ggc Phe Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly 320 325 330 335	1008
tcg ctg ggt gag cag cag tac tcg gtg ccg ccc ccg gtc tat ggc tgc Ser Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys 340 345 350	1056
cac acc ccc acc gac agc tgc acc ggc agc cag gct ttg ctg ctg agg His Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg 355 360 365	1104
acg ccc tac agc agt gac aat tta tac caa atg aca tcc cag ctt gaa Thr Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu 370 375 380	1152
tgc atg acc tgg aat cag atg aac tta gga gcc acc tta aag ggc cac Cys Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His 385 390 395	1200
agc aca ggg tac gag agc gat aac cac aca acg ccc atc ctc tgc gga Ser Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly 400 405 410 415	1248
gcc caa tac aga ata cac acg cac ggt gtc ttc aga ggc att cag gat Ala Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp 420 425 430	1296
gtg cga cgt gtg cct gga gta gcc ccg act ctt gta cggt gca tct Val Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser 435 440 445	1344
gag acc agt gag aaa cgc ccc ttc atg tgt gct tac tca ggc tgc aat Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn 450 455 460	1392
aag aga tat ttt aag ctg tcc cac tta cag atg cac agc agg aag cac Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His 465 470 475	1440

act ggt gag aaa cca tac cag tgc gac ttc aag gac tgt gaa cga agg		1488	
Thr Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg			
480	485	490	495
ttt ttt cgt tca gac cag ctc aaa aga cac caa agg aga cat aca ggt		1536	
Phe Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly			
500	505	510	
gtg aaa cca ttc cag tgc aaa act tgt cag cga aag ttc tcc cggt tcc		1584	
Val Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser			
515	520	525	
gac cac ctg aag acc cac acc agg act cat aca ggt gaa aag ccc ttc		1632	
Asp His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe			
530	535	540	
agc tgt cgg tgg cca agt tgt cag aaa aag ttt gcc cgg tca gat gaa		1680	
Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu			
545	550	555	
tta gtc cgc cat cac aac atg cat cag aga aac atg acc aaa ctc cag		1728	
Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln			
560	565	570	575
ctg gcg ctt tga gaattc		1746	
Leu Ala Leu			

<210> 8
 <211> 578
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: Ra12-WT1 fusion
 polypeptide

<400> 8			
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu			
1	5	10	15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala			
20	25	30	
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile			
35	40	45	
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn			
50	55	60	
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ser Leu			
65	70	75	80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile			
85	90	95	
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly			
100	105	110	
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr			
115	120	125	
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val			
130	135	140	
Pro Arg Gly Ser Pro Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu			
145	150	155	160
Leu Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Cys Ala Leu Pro			
165	170	175	
Val Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro			
180	185	190	

Gly Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala
195 200 205
Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu
210 215 220
Pro Ser Trp Gly Gly Ala Glu Pro His Glu Gln Cys Leu Ser Ala
225 230 235 240
Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys
245 250 255
Arg Tyr Gly Pro Phe Gly Pro Pro Ser Gln Ala Ser Ser Gly
260 265 270
Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu
275 280 285
Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp
290 295 300
Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln Phe
305 310 315 320
Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser
325 330 335
Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys His
340 345 350
Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr
355 360 365
Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys
370 375 380
Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His Ser
385 390 395 400
Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala
405 410 415
Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val
420 425 430
Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu
435 440 445
Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn Lys
450 455 460
Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His Thr
465 470 475 480
Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe
485 490 495
Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val
500 505 510
Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp
515 520 525
His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe Ser
530 535 540
Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu Leu
545 550 555 560
Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu
565 570 575
Ala Leu

<210> 9
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ra12-human gammaglobin fusion

<210> 10
<211> 220
<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:Ra12-human gammaglobin fusion polypeptide

<400> 10

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
35 40 45
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
50 55 60
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65 70 75 80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu Gly
130 135 140
Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr Ile
145 150 155 160
Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu Phe
165 170 175
Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys
180 185 190
Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met
195 200 205
Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
210 215 220

<210> 11

<211> 2191

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12-H9-32A fusion
(Ra12-MTB39-MTB32A(N-ter) fusion)

<220>

<221> CDS

<222> (1)..(2190)

<223> Ra12-H9-32A (Ra12-MTB39-MTB32A(N-ter)) fusion polypeptide

<400> 11

atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag ctg 48
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
1 5 10 15

tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg 96
Ser Gln Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
20 25 30

agt ggt gtg ctg cgt gtt ccg cca tat gtg atg ccg cat tct Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser	515 520 525	1584
ccg gca gcc ggc gat atc gcc ccg ccg gcc ttg tcg cag gac ccg ttc Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe	530 535 540	1632
gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln	545 550 555 560	1680
gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn	565 570 575	1728
gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val	580 585 590	1776
ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat gcg ttc Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe	595 600 605	1824
agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg tat gac Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp	610 615 620	1872
cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu	625 630 635 640	1920
ccg tcg gcg ggc atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val	645 650 655	1968
gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct Ala Met Gly Asn Ser Gly Gly Gln Gly Thr Pro Arg Ala Val Pro	660 665 670	2016
ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat tcg ctg Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu	675 680 685	2064
acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat gcc gcg Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala	690 695 700	2112
atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta gga cag Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln	705 710 715 720	2160
gtg gtc ggt atg aac acg gcc gcg tcc tag g Val Val Gly Met Asn Thr Ala Ala Ser	725 730	2191

<210> 12
 <211> 729
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:Ra12-H9-32A fusion
 polypeptide (Ra12-MTB39-MTB32A(N-ter) fusion polypeptide)

<400>	12		
Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu			
1	5	10	15
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala			
20	25	30	
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile			
35	40	45	
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn			
50	55	60	
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu			
65	70	75	80
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile			
85	90	95	
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly			
100	105	110	
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr			
115	120	125	
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp			
130	135	140	
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly			
145	150	155	160
Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val			
165	170	175	
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp			
180	185	190	
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val			
195	200	205	
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln			
210	215	220	
Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu			
225	230	235	240
Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg			
245	250	255	
Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr			
260	265	270	
Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln			
275	280	285	
Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr			
290	295	300	
Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly			
305	310	315	320
Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala			
325	330	335	
Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu			
340	345	350	
Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu			
355	360	365	
Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser			
370	375	380	
Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr			
385	390	395	400
Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala			
405	410	415	

Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 13
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: oligonucleotide
 primer for PCR amplification of Ra12 C-terminal
 fragment of MTB32A

<400> 13
 caattacata tgcatacacca tcaccatcac acggccgcgt ccgataactt c

51

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3'
oligonucleotide primer for PCR amplification of
Ra12 C-terminal fragment of MTB32A

<400> 14
ctaatcgaat tcggccgggg gtccctcgac caa

33

<210> 15
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'
oligonucleotide primer containing enterokinase
recognition site for PCR amplification of DPPD
mature secreted form

<400> 15
caattagaat tcgacgacga cgacaaggat ccacctgacc cgcatcag

48

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3'
oligonucleotide primer containing enterokinase
recognition site for PCR amplification of DPPD
mature secreted form

<400> 16
caattagaat tctcagggag cgttgggctg ctc

33

<210> 17
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12(short)
polypeptide

<400> 17
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
20 25 30

<210> 18
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Ra12(long)
polypeptide

<400> 18
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
20 25 30
Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
35 40 45
Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
50 55 60
Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
65 70 75 80
Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
85 90 95
Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
100 105 110
Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
115 120 125

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:5'
oligonucleotide primer, HindIII site, for PCR
amplification of human gammaglobin

<400> 19
gcgaagctta tgaagttgct gatggtcctc atgc 34

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3'
oligonucleotide primer, XhoI site, for PCR
amplification of human gammaglobin

<400> 20
cggtcgagt taaaataaat cacaaggact gctgtc 36

<210> 21
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
Met His His His His His
1 5

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: enterokinase
recognition site

<400> 22
Asp Asp Asp Lys
1

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

<210> 3
 <211> 396
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ral2

<220>
 <221> CDS
 <222> (1)..(396)
 <223> Ral2

<400> 3
 acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg|cag gga ttc 48
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15

gcc att ccg atc ggg cag gcg atg gcg atc ggc cag atc cga tcg		96	
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser			
20	25	30	
ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc		144	
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly			
35	40	45	
ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg		192	
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val			
50	55	60	
gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg		240	
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val			
65	70	75	80
atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg		288	
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala			
85	90	95	
gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg		336	
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp			
100	105	110	
caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag		384	
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu			
115	120	125	
gga ccc ccg gcc		396	
Gly Pro Pro Ala			
130			
<210> 4			
<211> 132			
<212> PRT			
<213> Mycobacterium tuberculosis			
<220>			
<223> 14 KD C-terminal fragment of MTB32A Ra12			
<400> 4			
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe			
1	5	10	15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser			
20	25	30	
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly			
35	40	45	
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val			
50	55	60	
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val			
65	70	75	80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala			
85	90	95	
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp			
100	105	110	
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu			
115	120	125	
Gly Pro Pro Ala			
130			

<400> 17
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
20 25 30

<210> 18
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ra12 (long) *full long R*
polypeptide

<400> 18
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
20 25 30
Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
35 40 45
Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
50 55 60
Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
65 70 75 80
Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
85 90 95
Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
100 105 110
Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
115 120 125

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5'
oligonucleotide primer, HindIII site, for PCR
amplification of human gammaglobin

<400> 19
gcgaagctta tgaagttgct gatggccctc atgc

34

<210> 20
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3'
oligonucleotide primer, XhoI site, for PCR
amplification of human gammaglobin

<400> 20
cggctcgagt taaaataaat cacaaggact gctgtc

36

```

<210> 21
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
Met His His His His His
    1          5

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:enterokinase
      recognition site

<400> 22
Asp Asp Asp Lys
    1

<210> 23
<211> 128
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> positions 1-128 of Ra12

<400> 23
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
    1           5           10           15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
    20          25          30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
    35          40          45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
    50          55          60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
    65          70          75          80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
    85          90          95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
    100         105         110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu ← NO:4 + GLyP, Pro Ala
    115         120         125

```